

### **AMENDMENTS TO THE CLAIMS:**

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1-35 (Cancelled).

36 (New). An amino acid selected from the group consisting of:

- (i) an amino acid having the sequence of SEQ ID NO:12;
- (ii) fragments of the amino acid of (i) having at least 10 amino acids;
- (iii) analogues of the amino acids of (i) or (ii) in which one or more amino acids has been added, deleted, replaced, or chemically modified without substantially altering the biological activity of the parent amino acid.

37(New). A method for identifying candidate compounds capable of binding to a KLK-2 variant product and modulating its activity the method comprising:

- (i) providing an amino acid as claimed in claim 36;
- (ii) contacting a candidate compound with said amino acid;
- (iii) determining the effect of said candidate compound on the biological activity of said amino acid; and
- (iv) selecting those compounds that show a significant effect on said biological activity.

38 (New). A method according to Claim 37, wherein the compound is an activator and the measured effect is increase in the biological activity.

39 (New). A method according to Claim 37, wherein the compound is a deactivator and the effect is decrease in the biological activity.

40 (New). A method for determining the level of amino acid sequences of KLK-2 variants in a biological sample comprising:

- (a) providing a biological sample containing an amino acid as claimed in claim 36;
- (b) contacting said biological sample with an antibody specific for the amino acid, thereby forming an antibody-antigen complex;
- (c) detecting the amount of antibody-antigen complex; and
- (d) normalizing the amount to provide the level of the amino acid sequences of KLK-2 variants in the sample.

41 (New). A method for determining the ratio between the level of any one of the amino acids of claim 36 of the KLK-2 variant present in a first biological sample and the level of the native KLK-2 sequence from which the variant has been varied by alternative splicing, in a second biological sample comprising:

- (a) determining the level of the KLK-2 variant amino acid sequence in the first biological sample according to the method of Claim 40;
- (b) determining the level of the KLK-2 native sequence in the second biological sample; and
- (c) comparing the levels obtained in (a) and (b) to give said ratio.

42 (New). A method according to Claim 41, wherein said first and said second biological samples are the same sample.

43 (New.) A method according to any one of Claims 40 to 42 for detecting the presence of prostate cancer or detecting pre-disposition to prostate cancer, or for detection of the malignancy of prostate cancer.